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RAW SEQUENCE LISTING

DATE: 05/07/2002

PATENT APPLICATION: US/09/835,976B

TIME: 13:57:30

Input Set : A:\EP.txt

Output Set: N:\CRF3\05072002\I835976B.raw

ENTERED

3 <110> APPLICANT: Mount, David B.
 4 Delpire, Eric
 5 Gamba, Gerardo
 6 Alfred L. George, Jr.
 8 <120> TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER
 NUCLEIC ACIDS AND
 9 POLYPEPTIDES AND
 10 THERAPEUTIC AND SCREENING METHODS USING SAME
 12 <130> FILE REFERENCE: Attorney Docket No. 1242-26-2
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/835,976B
 15 <141> CURRENT FILING DATE: 2001-04-16
 17 <160> NUMBER OF SEQ ID NOS: 131
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 5239
 23 <212> TYPE: DNA
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 31 <221> NAME/KEY: misc_feature
 32 <222> LOCATION: (161)
 33 <223> OTHER INFORMATION: n=a or c, Xaa=Leu or Ile
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 38 <223> OTHER INFORMATION: n=a or t, Xaa=Leu or Ile
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 51 ggc ggc ggc gac gag act gcc gag cgg acg gag gct ccg ggc acc ccc 97
 52 Gly Gly Gly Asp Glu Thr Ala Glu Arg Thr Glu Ala Pro Gly Thr Pro
 53 20 25 30
 55 gag ggc ccc gag ccc gag cgc ccc agc ccg gga gat gga aat cca aga 145
 56 Glu Gly Pro Glu Pro Glu Arg Pro Ser Pro Gly Asp Gly Asn Pro Arg
 57 35 40 45
 58 gaa aac agc cca ttc ntc aac aat gtc gag gtg gaa caa gag agc ttc 193
 59 Glu Asn Ser Pro Phe Xaa Asn Asn Val Glu Val Glu Gln Glu Ser Phe

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61 50 55 60

63 ttt gaa ggg aag aac atg gca ctt ttc gag gag gag atg gac agt aac 241

64 Phe Glu Gly Lys Asn Met Ala Leu Phe Glu Glu Glu Met Asp Ser Asn

65 65 70 75

67 ccc atg gtg tcc tcg ctg ntc aac aag ctg gcc aac tac acc aac ctg 289

68 Pro Met Val Ser Ser Leu Xaa Asn Lys Leu Ala Asn Tyr Thr Asn Leu

69 80 85 90 95

71 agc cag ggc gtg gtg gag cac gag gag gac gag gag agc cgg cgg cgg 337

72 Ser Gln Gly Val Val Glu His Glu Glu Asp Glu Glu Ser Arg Arg Arg

73 100 105 110

75 gag gcc aag gct ccg cgc atg ggc acc ttc atc ggc gtc tac ctg ccg 385

76 Glu Ala Lys Ala Pro Arg Met Gly Thr Phe Ile Gly Val Tyr Leu Pro

77 115 120 125

79 tgc ctg cag aac atc ctg ggc gtc atc ctc ttc ctg cgc ctg acg tgg 433

80 Cys Leu Gln Asn Ile Leu Gly Val Ile Leu Phe Leu Arg Leu Thr Trp

81 130 135 140

83 atc gtg ggg gtg gct ggt gtc ctg gag tcc ttc ctc atc gtg gcc atg 481

84 Ile Val Gly Val Ala Gly Val Leu Glu Ser Phe Leu Ile Val Ala Met

85 145 150 155

87 tgc tgc aca tgt aca atg ctg acc gcc att tcc atg agt gcg atc gct 529

88 Cys Cys Thr Cys Thr Met Leu Thr Ala Ile Ser Met Ser Ala Ile Ala

89 160 165 170 175

91 acc aac ggt gtg gtc cca gct ggc ggg tcc tac tac atg ata tcg cgc 577

92 Thr Asn Gly Val Val Pro Ala Gly Gly Ser Tyr Tyr Met Ile Ser Arg

93 180 185 190

95 tcg ctg gga ccc gag ttt gga ggc gct gtc ggc ctc tgc ttc tac ctg 625

96 Ser Leu Gly Pro Glu Phe Gly Gly Ala Val Gly Leu Cys Phe Tyr Leu

97 195 200 205

99 ggc acg acg ttt gca ggg gcc atg tat att ttg ggg acc atc gag att 673

100 Gly Thr Thr Phe Ala Gly Ala Met Tyr Ile Leu Gly Thr Ile Glu Ile

101 210 215 220

103 ttt ctg acg tac atc tcc ccg ggt gcg gcc atc ttc cag gcg gag gct 721

104 Phe Leu Thr Tyr Ile Ser Pro Gly Ala Ala Ile Phe Gln Ala Glu Ala

105 225 230 235

107 gca ggt ggc gag gcg gcc gcc atg ctg cac aac atg cgt gtg tac gcc 769

108 Ala Gly Gly Glu Ala Ala Met Leu His Asn Met Arg Val Tyr Gly

109 240 245 250 255

111 acg tgc acg ctc gtg ctc atg gcc ctg gtg gtc ttc gtg ggc gtc aag 817

112 Thr Cys Thr Leu Val Leu Met Ala Leu Val Val Phe Val Gly Val Lys

113 260 265 270

115 tat gtc aac aag ctg gcg ctg gtc ttc ctg gcc tgc gtc gtg ctg tcc 865

116 Tyr Val Asn Lys Leu Ala Leu Val Phe Leu Ala Cys Val Val Leu Ser

117 275 280 285

119 atc ctg gcc atc tat gcc ggc gtc atc aag tct gcc ttc gac ccc ccg 913

120 Ile Leu Ala Ile Tyr Ala Gly Val Ile Lys Ser Ala Phe Asp Pro Pro

121 290 295 300

123 gac atc ccg gtc tgc ctc ctg ggg aac cgc acg ctg tca cgg cgc agc 961

124 Asp Ile Pro Val Cys Leu Leu Gly Asn Arg Thr Leu Ser Arg Arg Ser

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127 ttc gat gcc tgc gtc aag gcc tac ggc atc cac aac aac tca gcc acc 1009
128 Phe Asp Ala Cys Val Lys Ala Tyr Gly Ile His Asn Asn Ser Ala Thr
129 320 325 330 335
131 tcc gcg ctc tgg ggc ctc ttc tgc aac ggc tcc cag ccc agc gcc gcc 1057
132 Ser Ala Leu Trp Gly Leu Phe Cys Asn Gly Ser Gln Pro Ser Ala Ala
133 340 345 350
135 tgt gac gag tac ttc atc cag aac aac gtc acc gaa atc cag ggc atc 1105
136 Cys Asp Glu Tyr Phe Ile Gln Asn Asn Val Thr Glu Ile Gln Gly Ile
137 355 360 365
139 ccg ggc gcg gcc agt ggt gtc ttc ctg gag aac ctg tgg agt acg tac 1153
140 Pro Gly Ala Ala Ser Gly Val Phe Leu Glu Asn Leu Trp Ser Thr Tyr
141 370 375 380
143 gcg cac gcg ggg gcg ttt gtg gag aag aaa ggt gtg ccc tcg gtg ccc 1201
144 Ala His Ala Gly Ala Phe Val Glu Lys Lys Gly Val Pro Ser Val Pro
145 385 390 395
147 gtg gca gag gag agc cgt gcc agc aca ctg ccc tac gtg ctc acc gac 1249
148 Val Ala Glu Glu Ser Arg Ala Ser Thr Leu Pro Tyr Val Leu Thr Asp
149 400 405 410 415
151 atc gcg gcc tcc ttc acc ctg ctg gtt ggc atc tac ttc cct tcc gtg 1297
152 Ile Ala Ala Ser Phe Thr Leu Leu Val Gly Ile Tyr Phe Pro Ser Val
153 420 425 430
155 acc ggt atc atg gcg ggt tca aac cgg tcc ggg gac ctc aag gat gca 1345
156 Thr Gly Ile Met Ala Gly Ser Asn Arg Ser Gly Asp Leu Lys Asp Ala
157 435 440 445
159 cag aag tcc atc ccc acg ggg acc atc ctg gcc ata gtg acg acg tct 1393
160 Gln Lys Ser Ile Pro Thr Gly Thr Ile Leu Ala Ile Val Thr Thr Ser
161 450 455 460
163 ttc atc tat ctc tcc tgc att gtg ctg ttt ggg gcc tgc att gaa ggc 1441
164 Phe Ile Tyr Leu Ser Cys Ile Val Leu Phe Gly Ala Cys Ile Glu Gly
165 465 470 475
167 gtg gtc tta cga gat aag ttc ggg gag gcc ctg cag ggg aac ctg gtc 1489
168 Val Val Leu Arg Asp Lys Phe Gly Glu Ala Leu Gln Gly Asn Leu Val
169 480 485 490 495
171 atc ggc atg ctg gcc tgg ccc tcc ccc tgg gtc atc gtc atc ggc tcc 1537
172 Ile Gly Met Leu Ala Trp Pro Ser Pro Trp Val Ile Val Ile Gly Ser
173 500 505 510
175 ttc ttc tcc acc tgc ggt gcc ggc ctg cag acc ctc acg ggg gca ccg 1585
176 Phe Phe Ser Thr Cys Gly Ala Gly Leu Gln Thr Leu Thr Gly Ala Pro
177 515 520 525
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180 Arg Leu Leu Gln Ala Ile Ala Arg Asp Gly Ile Val Pro Phe Leu Gln
181 530 535 540
183 gtg ttt ggc cac ggg aag gcc aac ggg gag ccc acg tgg gcg ctg ctg 1681
184 Val Phe Gly His Gly Lys Ala Asn Gly Glu Pro Thr Trp Ala Leu Leu
185 545 550 555
187 ctg aca gtc ctc atc tgc gag act ggc atc ctc atc gcc tct ctg gac 1729
188 Leu Thr Val Leu Ile Cys Glu Thr Gly Ile Leu Ile Ala Ser Leu Asp
189 560 565 570 575
191 agc gtg gcc ccg atc ctc tcc atg ttc ttc ctc atg tgc tac ctg ttc 1777

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193					580					585					590		
195	gtg	aac	ctg	gcc	tgc	gcc	gtg	cag	acc	ctg	cta	cgt	acc	ccc	aac	tgg	1825
196	Val	Asn	Leu	Ala	Cys	Ala	Val	Gln	Thr	Leu	Leu	Arg	Thr	Pro	Asn	Trp	
197				595					600					605			
199	cgt	cca	cgc	ttc	aag	ttc	tac	cac	tgg	acc	ctg	tcc	ttt	ctg	ggt	atg	1873
200	Arg	Pro	Arg	Phe	Lys	Phe	Tyr	His	Trp	Thr	Leu	Ser	Phe	Leu	Gly	Met	
201			610					615					620				
203	agc	ctg	tgc	ctg	gcg	ctg	atg	ttc	atc	tgc	tcc	tgg	tac	tac	gcg	ctg	1921
204	Ser	Leu	Cys	Leu	Ala	Leu	Met	Phe	Ile	Cys	Ser	Trp	Tyr	Tyr	Ala	Leu	
205		625					630					635					
207	tcc	gcc	atg	ctc	atc	gct	ggc	tgc	atc	tac	aag	tac	atc	gag	tac	cgc	1969
208	Ser	Ala	Met	Leu	Ile	Ala	Gly	Cys	Ile	Tyr	Lys	Tyr	Ile	Glu	Tyr	Arg	
209	640					645					650				655		
211	ggg	gcc	gag	aag	gag	tgg	ggc	gat	ggc	atc	cgt	ggc	cta	tcc	ctg	aac	2017
212	Gly	Ala	Glu	Lys	Glu	Trp	Gly	Asp	Gly	Ile	Arg	Gly	Leu	Ser	Leu	Asn	
213				660						665					670		
215	gcc	gcc	cgc	tac	gcc	ctg	ctg	cgc	gtg	gag	cac	ggt	ccc	ccc	cac	acc	2065
216	Ala	Ala	Arg	Tyr	Ala	Leu	Leu	Arg	Val	Glu	His	Gly	Pro	Pro	His	Thr	
217			675						680					685			
219	aag	aac	tgg	agg	ccc	cag	gtg	ctg	gtg	atg	ctg	aac	ctg	gac	gcg	gag	2113
220	Lys	Asn	Trp	Arg	Pro	Gln	Val	Leu	Val	Met	Leu	Asn	Leu	Asp	Ala	Glu	
221			690						695				700				
223	cag	gcc	gtg	aag	cac	ccc	cgc	ctg	ctg	tcc	ttc	acg	tcg	cag	ctg	aag	2161
224	Gln	Ala	Val	Lys	His	Pro	Arg	Leu	Leu	Ser	Phe	Thr	Ser	Gln	Leu	Lys	
225		705					710					715					
227	gcc	ggc	aag	ggc	ctg	acc	atc	gtg	ggc	tcg	gtg	ctg	gag	ggg	acg	tac	2209
228	Ala	Gly	Lys	Gly	Leu	Thr	Ile	Val	Gly	Ser	Val	Leu	Glu	Gly	Thr	Tyr	
229	720					725					730				735		
231	ctg	gac	aag	cac	atg	gag	gct	cag	cgg	gcc	gag	gag	aac	ata	cgg	tcc	2257
232	Leu	Asp	Lys	His	Met	Glu	Ala	Gln	Arg	Ala	Glu	Glu	Asn	Ile	Arg	Ser	
233				740						745					750		
235	cta	atg	agc	aca	gag	aag	acc	aag	ggc	ttc	tgc	cag	ctg	gtg	gtc	tcg	2305
236	Leu	Met	Ser	Thr	Glu	Lys	Thr	Lys	Gly	Phe	Cys	Gln	Leu	Val	Val	Ser	
237				755						760					765		
239	tcc	agc	ctg	cgg	gat	ggc	atg	tcc	cac	ctg	atc	cag	tcg	gcc	ggc	ctg	2353
240	Ser	Ser	Leu	Arg	Asp	Gly	Met	Ser	His	Leu	Ile	Gln	Ser	Ala	Gly	Leu	
241			770					775						780			
243	ggc	ggc	ctg	aag	cac	aac	acg	gtg	ctc	atg	gcc	tgg	ccc	gca	tcc	tgg	2401
244	Gly	Gly	Leu	Lys	His	Asn	Thr	Val	Leu	Met	Ala	Trp	Pro	Ala	Ser	Trp	
245		785					790					795					
247	aag	cag	gag	gac	aac	ccc	ttc	tcc	tgg	aag	aac	ttt	gta	gac	acc	gtc	2449
248	Lys	Gln	Glu	Asp	Asn	Pro	Phe	Ser	Trp	Lys	Asn	Phe	Val	Asp	Thr	Val	
249	800					805					810				815		
251	cgc	gac	acc	acc	gcc	gcg	cac	cag	gct	ctg	ctg	gtg	gcc	aag	aac	gtc	2497
252	Arg	Asp	Thr	Thr	Ala	Ala	His	Gln	Ala	Leu	Leu	Val	Ala	Lys	Asn	Val	
253				820						825					830		
255	gac	tcg	ttt	ccg	caa	aac	cag	gag	cgc	ttc	ggc	ggg	ggc	cac	atc	gac	2545
256	Asp	Ser	Phe	Pro	Gln	Asn	Gln	Glu	Arg	Phe	Gly	Gly	Gly	His	Ile	Asp	

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257 835 840 845
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 260 Val Trp Trp Ile Val His Asp Gly Gly Met Leu Met Leu Leu Pro Phe
 261 850 855 860
 263 ctg ctg cgc cag cac aag gtg tgg agg aag tgc cgg atg cgt atc ttc 2641
 264 Leu Leu Arg Gln His Lys Val Trp Arg Lys Cys Arg Met Arg Ile Phe
 265 865 870 875
 267 acc gtg gcc cag gtg gac gac aac agc atc cag atg aag aag gac ctg 2689
 268 Thr Val Ala Gln Val Asp Asp Asn Ser Ile Gln Met Lys Lys Asp Leu
 269 880 885 890 895
 271 cag atg ttc ttg tat cac ttg cgc atc agc gcc gag gtg gag gtg gtg 2737
 272 Gln Met Phe Leu Tyr His Leu Arg Ile Ser Ala Glu Val Glu Val Val
 273 900 905 910
 275 gag atg gtt gaa aac gac ata tct gct ttc acc tac gag agg aca cta 2785
 276 Glu Met Val Glu Asn Asp Ile Ser Ala Phe Thr Tyr Glu Arg Thr Leu
 277 915 920 925
 279 atg atg gag cag agg tcg cag atg ctg aag cag atg cag ctg tcc aag 2833
 280 Met Met Glu Gln Arg Ser Gln Met Leu Lys Gln Met Gln Leu Ser Lys
 281 930 935 940
 283 aac gag cag gag cga gag gcc cag ctg atc cac gac agg aac acc gcg 2881
 284 Asn Glu Gln Glu Arg Glu Ala Gln Leu Ile His Asp Arg Asn Thr Ala
 285 945 950 955
 287 tcc cac acc gcg gcg gca gcc agg acc caa gcg ccg cct acg cca gac 2929
 288 Ser His Thr Ala Ala Ala Ala Arg Thr Gln Ala Pro Pro Thr Pro Asp
 289 960 965 970 975
 291 aag gtg cag atg acc tgg acc agg gag aag ctg atc gct gag aag tac 2977
 292 Lys Val Gln Met Thr Trp Thr Arg Glu Lys Leu Ile Ala Glu Lys Tyr
 293 980 985 990
 295 agg agc aga gac acc agc cta tcc ggt ttc aaa gac ctc ttc agc atg 3025
 296 Arg Ser Arg Asp Thr Ser Leu Ser Gly Phe Lys Asp Leu Phe Ser Met
 297 995 1000 1005
 299 aag ccg gac cag tcc aac gtc agg cgg atg cac acg gct gtg aag ctc 3073
 300 Lys Pro Asp Gln Ser Asn Val Arg Arg Met His Thr Ala Val Lys Leu
 301 1010 1015 1020
 303 aat ggc gtc gtc ntc aac aag tcc cag gat gcg cag ctg gtc ctg ctc 3121
 304 Asn Gly Val Val Xaa Asn Lys Ser Gln Asp Ala Gln Leu Val Leu Leu
 305 1025 1030 1035
 307 aac atg cca ggt cct ccc aaa aac cgg cag gga gac gag aac tac atg 3169
 308 Asn Met Pro Gly Pro Pro Lys Asn Arg Gln Gly Asp Glu Asn Tyr Met
 309 1040 1045 1050 1055
 311 gag ttt ctt gaa gtc ctg acc gag ggg ctg aac aga gtc ctc ctg gtc 3217
 312 Glu Phe Leu Glu Val Leu Thr Glu Gly Leu Asn Arg Val Leu Leu Val
 313 1060 1065 1070
 315 agg ggt ggc ggc cgg gag gtg atc acc atc tac tcc taatgcccaa 3263
 316 Arg Gly Gly Gly Arg Glu Val Ile Thr Ile Tyr Ser
 317 1075 1080
 319 cagcatcacg gcaactctggg acaggcacgg aggacggcgt gggcagcctg ggccctgggct 3323
 321 tggcccaggg aaccagacgg cagacacacc tgtccccag tgatgccacc caagctgccc 3383
 323 atggggcttc ctacggaagt ttctaggccc gtcacctagg gctctcctgt tcagccttaa 3443

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:1; Xaa Pos. 53,86,1028
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Seq#:3; N Pos. 267,1578,3387
Seq#:3; Xaa Pos. 35,472,1075
Seq#:4; Xaa Pos. 35,472,1075
Seq#:5; N Pos. 307,1894,3340
Seq#:5; Xaa Pos. 102,631,1113
Seq#:6; Xaa Pos. 102,631,1113
Seq#:7; N Pos. 106,925,2545
Seq#:7; Xaa Pos. 35,308,848
Seq#:9; N Pos. 284,1697,3008
Seq#:9; Xaa Pos. 66,537,974
Seq#:10; Xaa Pos. 66,537,974
Seq#:11; N Pos. 358,1072,2746
Seq#:11; Xaa Pos. 120,358,916
Seq#:12; Xaa Pos. 120,358,916
Seq#:13; N Pos. 283,535,1471,1828,1987,3139
Seq#:13; Xaa Pos. 71,155,467,586,639,1023
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Seq#:15; N Pos. 267,1200,2529
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Seq#:17; N Pos. 74,190
Seq#:18; N Pos. 525
Seq#:19; N Pos. 574
Seq#:46; N Pos. 294
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Seq#:112; N Pos. 1817,2113,2161
Seq#:131; N Pos. 636,637,638,639,640,1084

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:114; Line(s) 7030